

ALIGNMENTS

Sequence Comparison
"A"

RESULT 1

AAY99372

ID AAY99372 standard; Protein; 331 AA.

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AC AAY99372;

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DT 08-AUG-2000 (first entry)

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DE Human PRO1430. (UNQ736) amino acid sequence SEQ ID NO:116.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;

KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

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OS Homo sapiens.

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PN WO200012708-A2.

XX

PD 09-MAR-2000. ✓

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PF 01-SEP-1999; 99WO-US20111.

XX

PR 01-SEP-1998; 98US-0098716.

PR 01-SEP-1998; 98US-0098749.

PR 01-SEP-1998; 98US-0098750.

PR 02-SEP-1998; 98US-0098803.

PR 02-SEP-1998; 98US-0098821.

PR 02-SEP-1998; 98US-0098843.

PR 09-SEP-1998; 98US-0099536.

PR 09-SEP-1998; 98US-0099596.

PR 09-SEP-1998; 98US-0099598.

PR 09-SEP-1998; 98US-0099602.

PR 09-SEP-1998; 98US-0099642.

XX

PA (GETH) GENENTECH INC.

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PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

XX

DR WPI; 2000-237871/20.

DR

N-PSDB; AAA37054.

XX

PT New mammalian DNA sequences encoding transmembrane, receptor or

PT secreted PRO polypeptides, useful for screening of potential peptide or

PT small molecule inhibitors of the relevant receptor/ligand interactions

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PS Claim 12; Fig 66; 773pp; English.

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CC AAA37022 to AAA37144 encode the new isolated human transmembrane,

CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The

CC transmembrane and receptor PRO proteins can be used for screening of

CC potential peptide or small molecule inhibitors of the relevant

CC receptor/ligand interactions. The polypeptides and nucleotide sequences

CC encoding then have various industrial applications, including uses as

CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent

CC PCR primers and hybridisation probes used in the isolation of the PRO

CC polypeptides from the present invention.

XX

SQ Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 21; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-166;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60

Db 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60

QY 61 RGGNIILACRDMKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDI 120

Db 61 RGGNIILACRDMKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEERVDI 120

QY 121 LINNAGVMRCPHWTTEDGFEMQFGVNHGFLTNLLLDKLGKASAPSRIINLSSLAHVAG 180

Db 121 LINNAGVMRCPHWTTEDGFEMQFGVNHGFLTNLLLDKLGKASAPSRIINLSSLAHVAG 180

QY 181 HIDFDDLNWQTRKYNTKAAAYCQSKLAIVLFTKLSRRLQSGSVTVNALHPGVARTELRH 240

Db 181 HIDFDDLNWQTRKYNTKAAAYCQSKLAIVLFTKLSRRLQSGSVTVNALHPGVARTELRH 240

QY 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAOPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300

Db 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAOPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300

QY 301 EDEEVARRLWAEARLVGLEAPSVREQLPR 331

Db 301 EDEEVARRLWAEARLVGLEAPSVREQLPR 331

RESULT 2
AAE05174

ID AAE05174 standard; Protein; 331 AA.

AC AAE05174;

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DT 12-SEP-2001 (first entry)

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DE Human drug metabolising enzyme (DME-5) protein.

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KW Human; drug metabolising enzyme; DME-5; immunosuppressive; gene therapy;
cytostatic; autoimmune disorder; inflammatory disorder; atherosclerosis;
osteoporosis; eye disorder; hepatic tumour; Addison's disease; cretinism;
rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia;
developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy;
thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma;
gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma;
actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma;
cell proliferative disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide

1..17

FT

/label= Signal_peptide

FT

Protein

18..331

FT

/note= "Mature drug metabolising enzyme (DME-5) protein"

XX

PN WO200151638-A2.✓

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PD 19-JUL-2001.✓

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PF 12-JAN-2001; 2001WO-US01174.

XX

PR 14-JAN-2000; 2000US-0176139.

PR

21-JAN-2000; 2000US-0177443.

PR

28-JAN-2000; 2000US-0178574.

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PA (INCY-) INCYTE GENOMICS INC.

XX

PI Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R;

PI

Ring HZ, Hillman JL, Yue H, Azimzai Y, Yao MG, Gandhi AR;

PI

Nguyen DB, Tang YT, Lal P, Bandman O;

XX

DR WPI; 2001-425874/45.

DR

N-PSDB; AAD09940.

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PT Drug metabolizing enzymes and encoding polynucleotides, useful for
diagnosing, treating and/or preventing autoimmune, inflammatory, cell
proliferative, developmental, endocrine, eye, metabolic, and
gastrointestinal disorders -

PT

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PS Claim 1; Page 139-140; 133pp; English.

XX

CC The present sequence is human drug metabolising enzyme (DME-5) protein.

CC

CC Human DME and its nucleic acid molecule are useful for the diagnosis,

CC

CC treatment and prevention of disorders associated with increased or

CC

CC decreased expression of DME. Examples of such disorders include,

CC

CC autoimmune/inflammatory disorder such as acquired immune deficiency

CC

CC syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative

CC

CC disorder such as actinic keratosis, atherosclerosis; developmental

CC

CC disorder such as epilepsy, anaemia, endocrine disorder such as

CC

CC acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as

CC

CC diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis;

CC

CC metabolic disorder such as Addison's disease, obesity; gastrointestinal

CC

CC disorder such as anorexia, dysphagia and hepatic tumours including

CC

CC nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for

CC

CC creating 'knockin' humanised animals (pigs) or transgenic animals (mice

CC

CC or rats) to model human disease. DME DNA is also in useful is gene

CC

CC therapy. DME and its immunogenic fragments are useful for screening

CC

CC libraries of compounds in several drug screening assays.

XX

SQ

Sequence 331 AA;

Query Match 100.0%; Score 1695; DB 22; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-166;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60
Db 1 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELAR 60
Qy 61 RGGNIILACRDMKCEAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEERVDI 120
Db 61 RGGNIILACRDMKCEAAKDIRGETLNHHVNAHRLDLASLKSIREFAAKIIEEERVDI 120
Qy 121 LINNAGVMRCPHWTTEDGFEMQFGVNHGLHPLLNLNLLDKLKASAPSRIINLSSLAHVAG 180
Db 121 LINNAGVMRCPHWTTEDGFEMQFGVNHGLHPLLNLNLLDKLKASAPSRIINLSSLAHVAG 180
Qy 181 HIDPDDLNWQTRKYNTKAAAYCQSKLAIVLPTKELSRRLQSGSVTVNALHPGVARTELRH 240
Db 181 HIDPDDLNWQTRKYNTKAAAYCQSKLAIVLPTKELSRRLQSGSVTVNALHPGVARTELRH 240
Qy 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
Db 241 TGIHGSTFSSTTLGPIFWLLVKSPELAAPSTYLAVAEELADVSGKYFDGLKQKAPAPEA 300
Qy 301 EDEEVARRLWABESARLVGLEAPSVREQPLPR 331
Db 301 EDEEVARRLWABESARLVGLEAPSVREQPLPR 331